Sequence Listing

<110> Reilly, Dorothea
Yansura, Daniel G.

<120> METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

<130> 11669.195USU1

<140> US 10/697,995
<141> 2003-10-30

<150> US 60/422,952
<151> 2002-10-31

<160> 37

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<223> anti-TF vector

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atagtcgctt tgtttttatt ttttaatgta tttgtaacta gtacgcaagt 400

tcacgtaaaa agggtatcta gaattatgaa gaagaatatc gcatttcttc 450

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caccatcacc tgcagagcca gtcgcgacat caagagctat ctgaactggt 600

atcaacagaa accaggaaaa gctccgaaag tactgattta ctatgctact 650

agtctcgctg aaggagtccc ttctcgcttc tctggatccg gttctgggac 700

ggattacact ctgaccatca gcagtctgca gccagaagac ttcgcaactt 750

attactgtct tcagcacgga gagtctccat ggacatttgg acagggtacc 800

aaggtggaga tcaaacgaac tgtggctgca ccatctgtct tcatcttccc 850

gccatctgat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc 900

tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000

ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 1050

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tgcatctatg ttcgtttttt ctattgctac aaacgcgtac gctgaggttc 1650

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ttaaattgct aacgcagtca ggcaccgtgt atgaaatcta acaatgcgct 3150

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<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-TF light chain

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                20                  25                  30

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                35                  40                  45

Cys Arg Ala Ser Arg Asp Ile Lys Ser Tyr Leu Asn Trp Tyr Gln
                50                  55                  60

Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Tyr Ala Thr
                65                  70                  75

Ser Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
                80                  85                  90

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                95                 100                 105

Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Trp Thr
               110                 115                 120

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
               125                 130                 135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
               140                 145                 150

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
               155                 160                 165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
               170                 175                 180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
               185                 190                 195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
               200                 205                 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
               215                 220                 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
               230                 235
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<210> 3
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-TF heavy chain

<400> 3

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Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
                20                  25                  30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                35                  40                  45

Ala Ala Ser Gly Phe Asn Ile Lys Glu Tyr Tyr Met His Trp Val
                50                  55                  60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Leu Ile Asp
                65                  70                  75

Pro Glu Gln Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln Asp Arg
                80                  85                  90

Ala Thr Ile Ser Ala Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                95                 100                 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
               110                 115                 120

Arg Asp Thr Ala Ala Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
               125                 130                 135

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
               140                 145                 150

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
               155                 160                 165

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
               170                 175                 180

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
               185                 190                 195

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
               200                 205                 210

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
               215                 220                 225

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
               230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
               245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
               260                 265                 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
               275                 280                 285
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Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
320 325 330

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
335 340 345

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
350 355 360

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
365 370 375

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
380 385 390

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
395 400 405

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
410 415 420

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
425 430 435

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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Leu Ser Pro Gly Lys
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<211> 3242
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-TF vector

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tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200

gggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250

gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300

aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt 350

atagtcgctt tgtttttatt ttttaatgta tttgtaacta gtacgcaagt 400

tcacgtaaaa agggtatcta gaattatgaa gaaaaacatc gcttttcttc 450

ttgcatctat gttcgttttt tctattgcta caaacgcgta cgctgatatc 500

cagatgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550

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<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF light chain

<400> 5

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				20				25						30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
				35				40						45	
Cys	Arg	Ala	Ser	Arg	Asp	Ile	Lys	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln
				50				55						60	
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Tyr	Ala	Thr
				65				70						75	
Ser	Leu	Ala	Glu	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
				80				85						90	
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
				95				100						105	
Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	His	Gly	Glu	Ser	Pro	Trp	Thr
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Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
				125				130						135	
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
				140				145						150	
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
				155				160						165	
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
				170				175						180	

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Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                185                 190                 195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
                200                 205                 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                215                 220                 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                230                 235
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<210> 6
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF heavy chain

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Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                35                  40                  45

Ala Ala Ser Gly Phe Asn Ile Lys Glu Tyr Tyr Met His Trp Val
                50                  55                  60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Leu Ile Asp
                65                  70                  75

Pro Glu Gln Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln Asp Arg
                80                  85                  90

Ala Thr Ile Ser Ala Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                95                 100                 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                110                 115                 120

Arg Asp Thr Ala Ala Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                125                 130                 135

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                140                 145                 150

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                155                 160                 165

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                170                 175                 180
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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                185                 190                 195

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                200                 205                 210

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
                215                 220                 225

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
                230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                260                 265                 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                305                 310                 315

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                320                 325                 330

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                335                 340                 345

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                350                 355                 360

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                365                 370                 375

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                380                 385                 390

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                395                 400                 405

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                410                 415                 420

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                425                 430                 435

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                440                 445                 450

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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455 460 465

Leu Ser Pro Gly Lys
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<210> 7
<211> 3300
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-VEGF vector

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tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200

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gccatctgat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc 900

tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000

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tgcatctatg ttcgtttttt ctattgctac aaacgcgtac gctgaggttc 1650

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acggcacgag ccactggtat ttcgacgtct ggggtcaagg aaccctggtc 2000

accgtctcct cggcctccac caagggccca tcggtcttcc ccctggcacc 2050

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<210> 8
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-VEGF light chain

<400> 8

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				20				25						30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
				35				40						45	
Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	
				50				55						60	
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Phe	Thr	Ser	

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                65                  70                  75

Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
                80                  85                  90

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                95                 100                 105

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp Thr
               110                 115                 120

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
               125                 130                 135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
               140                 145                 150

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
               155                 160                 165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
               170                 175                 180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
               185                 190                 195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
               200                 205                 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
               215                 220                 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
               230                 235

<210> 9
<211> 476
<212> PRT
<213> Artificial Sequence

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 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
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 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                35                  40                  45

 Ala Ala Ser Gly Tyr Asp Phe Thr His Tyr Gly Met Asn Trp Val
                50                  55                  60
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Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Trp Ile Asn
                65                  70                  75

Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe Lys Arg Arg
                80                  85                  90

Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln
                95                 100                 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
               110                 115                 120

Lys Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp Val
               125                 130                 135

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
               140                 145                 150

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
               155                 160                 165

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
               170                 175                 180

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
               185                 190                 195

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
               200                 205                 210

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
               215                 220                 225

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
               230                 235                 240

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
               245                 250                 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
               260                 265                 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
               275                 280                 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
               290                 295                 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
               305                 310                 315

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
               320                 325                 330

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
               335                 340                 345
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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
350 355 360

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
365 370 375

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
380 385 390

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
395 400 405

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
410 415 420

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
425 430 435

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
440 445 450

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
455 460 465

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
470 475

<210> 10
<211> 3255
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-VEGF vector

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gaactgtgtg cgcaggtaga agctttggag attatcgtca ctgcaatgct 150

tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200

gggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250

gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300

aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt 350

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tcacgtaaaa agggtatcta gaattatgaa gaagaatatc gcatttcttc 450

ttgcatctat gttcgttttt tctattgcta caaacgcgta cgctgatatc 500

cagttgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550

caccatcacc tgcagcgcaa gtcaggatat tagcaactat ttaaactggt 600

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tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000

ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 1050

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accgtgtatg aaatctaaca atgcgctcat cgtcatcctc ggcaccgtca 3200

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<210> 11
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-VEGF light chain

<400> 11

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 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Leu Thr Gln Ser
                20                  25                  30

 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                35                  40                  45

 Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
                50                  55                  60

 Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Phe Thr Ser
                65                  70                  75

 Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
                80                  85                  90

 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                95                 100                 105

 Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp Thr
               110                 115                 120

 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
               125                 130                 135

 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
               140                 145                 150

 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
               155                 160                 165

 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
               170                 175                 180

 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
               185                 190                 195

 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
               200                 205                 210

 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
               215                 220                 225

 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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230 235

<210> 12
<211> 479
<212> PRT
<213> Artificial sequence

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<223> Anti-VEGF heavy chain

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Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
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Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
20 25 30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
35 40 45

Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Ile Asn Trp Val
50 55 60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Trp Ile Asn
65 70 75

Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe Lys Arg Arg
80 85 90

Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln
95 100 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
110 115 120

Lys Tyr Pro His Tyr Tyr Val Asn Glu Arg Lys Ser His Trp Tyr
125 130 135

Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
140 145 150

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
155 160 165

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
170 175 180

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
185 190 195

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
200 205 210

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
215 220 225

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Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
                230                 235                 240

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
                245                 250                 255

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                260                 265                 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                305                 310                 315

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                320                 325                 330

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                335                 340                 345

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
                350                 355                 360

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                365                 370                 375

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
                380                 385                 390

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                395                 400                 405

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                410                 415                 420

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                425                 430                 435

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                440                 445                 450

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                455                 460                 465

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 13
<211> 1139
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 13
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atcggaagct gtggtatggc tgtgcaggtc gtaaatcact gcataattcg 150

tgtcgctcaa ggcgcactcc cgttctggat aatgtttttt gcgccgacat 200

cataacggtt ctggcaaata ttctgaaatg agctgttgac aattaatcat 250

cgaactagtt taatgtgtgg aattgtgagc ggataacaat taagcttagg 300

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gaccacaatg gccgttgccc tgcatgcacc aatcactttt gctgctgaag 400

ctgcaaaacc tgctacagct gctgacagca aagcagcgtt caaaaatgac 450

gatcagaaat cagcttatgc actgggtgcc tcgctgggtc gttacatgga 500

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agctgatcgc tggtgttcag gatgcatttg ctgataagag caaactctcc 600

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gtaaagagta ccgcgagaaa tttgccaaag agaaaggtgt gaaaacctct 750

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ctgctggatg tgaaaccagc gccgaaggct gatgcaaagc cggaagctga 1100

tgcgaaagcc gcagattctg ctaaaaaata aaagctagc 1139

<210> 14
<211> 1139
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 14
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tagccttcga caccataccg acacgtccag catttagtga cgtattaagc 150

acagcgagtt ccgcgtgagg gcaagaccta ttacaaaaaa cgcggctgta 200

gtattgccaa gaccgtttat aagactttac tcgacaactg ttaattagta 250

gcttgatcaa attacacacc ttaacactcg cctattgtta attcgaatcc 300

taagatctcc cttctaaata ctttagtgac aaatttcatt gcgacgaccg 350

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catttctcat ggcgctcttt aaacggtttc tctttccaca cttttggaga 750

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tccgccattc tagtttgacc aataaggtgg tcttgaccga atgccgtttc 1000

gcccacaagg cccctagggt ggcttaagat gggaccacaa actgcatctc 1050

gacgacctac actttggtcg cggcttccga ctacgtttcg gccttcgact 1100

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<210> 15
<211> 270
<212> PRT
<213> E. coli

<400> 15
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Val Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys
                20                  25                  30

Pro Ala Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp
                35                  40                  45

Gln Lys Ser Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met
                50                  55                  60

Glu Asn Ser Leu Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp
                65                  70                  75

Lys Asp Gln Leu Ile Ala Gly Val Gln Asp Ala Phe Ala Asp Lys
                80                  85                  90

Ser Lys Leu Ser Asp Gln Glu Ile Glu Gln Thr Leu Gln Ala Phe
                95                 100                 105

Glu Ala Arg Val Lys Ser Ser Ala Gln Ala Lys Met Glu Lys Asp
               110                 115                 120

Ala Ala Asp Asn Glu Ala Lys Gly Lys Glu Tyr Arg Glu Lys Phe
               125                 130                 135

Ala Lys Glu Lys Gly Val Lys Thr Ser Ser Thr Gly Val Leu Tyr
               140                 145                 150

Gln Val Val Glu Ala Gly Lys Gly Glu Ala Pro Lys Asp Ser Asp
               155                 160                 165

Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile Asp Gly Lys Glu
               170                 175                 180

Phe Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser Phe Arg Leu
               185                 190                 195

Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn Ile Lys
               200                 205                 210

Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala Tyr
               215                 220                 225

Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val
               230                 235                 240

Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp
               245                 250                 255

Ala Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys
               260                 265                 270
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<210> 16
<211> 3000
<212> DNA

<213> Artificial sequence

<220>
<223> Anti-TF vector

<400> 16
gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatc 50

tcattgctga gttgttattt aagcttgccc aaaaagaaga agagtcgaat 100

gaactgtgtg cgcaggtaga agctttggag attatcgtca ctgcaatgct 150

tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200

gggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250

gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300

aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt 350

atagtcgctt tgtttttatt ttttaatgta tttgtaacta gtacgcaagt 400

tcacgtaaaa agggtatcta gaattatgaa aaagaatatc gcatttcttc 450

ttgcatctat gttcgttttt tctattgcta caaacgcgta cgctgatatc 500

cagatgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550

caccatcacc tgcagagcca gtcgcgacat caagagctat ctgaactggt 600

atcaacagaa accaggaaaa gctccgaaag tactgattta ctatgctact 650

agtctcgctg aaggagtccc ttctcgcttc tctggatccg gttctgggac 700

ggattacact ctgaccatca gcagtctgca gccagaagac ttcgcaactt 750

attactgtct tcagcacgga gagtctccat ggacatttgg acagggtacc 800

aaggtggaga tcaaacgaac tgtggctgca ccatctgtct tcatcttccc 850

gccatctgat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc 900

tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000

ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 1050

acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 1100

tcgcccgtca caaagagctt caacagggga gagtgttaat taaatcctct 1150

acgccggacg catcgtggcg agctcggtac ccggggatct aggcctaacg 1200

ctcggttgcc gccgggcgtt ttttattgtt gccgacgcgc atctcgactg 1250

cacggtgcac caatgcttct ggcgtcaggc agccatcgga agctgtggta 1300

tggctgtgca ggtcgtaaat cactgcataa ttcgtgtcgc tcaaggcgca 1350

ctcccgttct ggataatgtt ttttgcgccg acatcataac ggttctggca 1400

aatattctga aatgagctgt tgacaattaa tcatcgaact agtttaatgt 1450

gtggaattgt gagcggataa caattaagct taggatctag aattatgaag 1500

aagaatattg cgttcctact tgcctctatg tttgtctttt ctatagctac 1550

aaacgcgtac gctgaggttc agctggtgga gtctggcggt ggcctggtgc 1600

agccaggggg ctcactccgt ttgtcctgtg cagcttctgg cttcaatatt 1650

aaggagtact acatgcactg ggtccgtcag gccccgggta agggcctgga 1700

atgggttgga ttgattgatc cagagcaagg caacacgatc tatgacccga 1750

agttccagga ccgtgccact ataagcgctg acaattccaa aaacacagca 1800

tacctgcaga tgaacagcct gcgtgctgag gacactgccg tctattattg 1850

tgctcgagac acggccgctt acttcgacta ctggggtcaa ggaaccctgg 1900

tcaccgtctc ctcggcctcc accaagggcc catcggtctt ccccctggca 1950

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt 2000

caaggactac ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc 2050

tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 2100

tactccctca gcagcgtggt gactgtgccc tctagcagct tgggcaccca 2150

gacctacatc tgcaacgtga atcacaagcc cagcaacacc aaggtggaca 2200

agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 2250

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa 2300

acccaaggac accctcatga tctcccggac ccctgaggtc acatgcgtgg 2350

tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 2400

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta 2450

caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 2500

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 2550

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc 2600

acaggtgtac accctgcccc catcccggga agagatgacc aagaaccagg 2650

tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 2700

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc 2750

cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 2800

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 2850

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg 2900

taaataagca tgcgacggcc ctagagtccc taacgctcgg ttgccgccgg 2950

gcgtttttta ttgttaactc atgtttgaca gcttatcatc gataagcttt 3000

<210> 17
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF light chain

<400> 17

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1				5				10						15	
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser
				20				25						30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
				35				40						45	
Cys	Arg	Ala	Ser	Arg	Asp	Ile	Lys	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln
				50				55						60	
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Tyr	Ala	Thr
				65				70						75	
Ser	Leu	Ala	Glu	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
				80				85						90	
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
				95				100						105	
Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	His	Gly	Glu	Ser	Pro	Trp	Thr
				110				115						120	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
				125				130						135	
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
				140				145						150	
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
				155				160						165	

```
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                  170                 175                 180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                  185                 190                 195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
                  200                 205                 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                  215                 220                 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                  230                 235
```

<210> 18
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF heavy chain

<400> 18

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 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
   1               5                  10                  15

 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
                  20                  25                  30

 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                  35                  40                  45

 Ala Ala Ser Gly Phe Asn Ile Lys Glu Tyr Tyr Met His Trp Val
                  50                  55                  60

 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Leu Ile Asp
                  65                  70                  75

 Pro Glu Gln Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln Asp Arg
                  80                  85                  90

 Ala Thr Ile Ser Ala Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                  95                 100                 105

 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                 110                 115                 120

 Arg Asp Thr Ala Ala Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                 125                 130                 135

 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                 140                 145                 150

 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                 155                 160                 165
```

```
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                170                 175                 180

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                185                 190                 195

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                200                 205                 210

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
                215                 220                 225

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
                230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                260                 265                 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                305                 310                 315

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                320                 325                 330

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                335                 340                 345

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                350                 355                 360

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                365                 370                 375

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                380                 385                 390

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                395                 400                 405

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                410                 415                 420

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                425                 430                 435

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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440 445 450

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
455 460 465

Leu Ser Pro Gly Lys
470

<210> 19
<211> 3000
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-TF vector

<400> 19
gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatc 50

tcattgctga gttgttattt aagcttgccc aaaaagaaga agagtcgaat 100

gaactgtgtg cgcaggtaga agctttggag attatcgtca ctgcaatgct 150

tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200

gggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250

gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300

aaaagttaat cttttcaaca gctgtcataa agttgtcacg gccgagactt 350

atagtcgctt tgtttttatt ttttaatgta tttgtaacta gtacgcaagt 400

tcacgtaaaa agggtatcta gaattatgaa aaagaatatc gcatttcttc 450

ttgcatctat gttcgttttt tctattgcta caaacgcgta cgctgatatc 500

cagatgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550

caccatcacc tgcagagcca gtcgcgacat caagagctat ctgaactggt 600

atcaacagaa accaggaaaa gctccgaaag tactgattta ctatgctact 650

agtctcgctg aaggagtccc ttctcgcttc tctggatccg gttctgggac 700

ggattacact ctgaccatca gcagtctgca gccagaagac ttcgcaactt 750

attactgtct tcagcacgga gagtctccat ggacatttgg acagggtacc 800

aaggtggaga tcaaacgaac tgtggctgca ccatctgtct tcatcttccc 850

gccatctgat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc 900

tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000

ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 1050

acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 1100

tcgcccgtca caaagagctt caacagggga gagtgttaat taaatcctct 1150

acgccggacg catcgtggcg agctcggtac ccggggatct aggcctaacg 1200

ctcggttgcc gccgggcgtt ttttattgtt gccgacgcgc atctcgactg 1250

cacggtgcac caatgcttct ggcgtcaggc agccatcgga agctgtggta 1300

tggctgtgca ggtcgtaaat cactgcataa ttcgtgtcgc tcaaggcgca 1350

ctcccgttct ggataatgtt ttttgcgccg acatcataac ggttctggca 1400

aatattctga aatgagctgt tgacaattaa tcatcgaact agtttaatgt 1450

gtggaattgt gagcggataa caattaagct taggatctag aattatgaag 1500

aagaatattg cgttcctact tgcctctatg tttgtctttt ctatagctac 1550

aaacgcgtac gctgaggttc agctggtgga gtctggcggt ggcctggtgc 1600

agccaggggg ctcactccgt ttgtcctgtg cagcttctgg cttcaatatt 1650

aaggagtact acatgcactg ggtccgtcag gccccgggta agggcctgga 1700

atgggttgga ttgattgatc cagagcaagg caacacgatc tatgacccga 1750

agttccagga ccgtgccact ataagcgctg acaattccaa aaacacagca 1800

tacctgcaga tgaacagcct gcgtgctgag gacactgccg tctattattg 1850

tgctcgagac acggccgctt acttcgacta ctggggtcaa ggaaccctgg 1900

tcaccgtctc ctcggcctcc accaagggcc catcggtctt ccccctggca 1950

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt 2000

caaggactac ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc 2050

tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 2100

tactccctca gcagcgtggt gactgtgccc tctagcagct tgggcaccca 2150

gacctacatc tgcaacgtga atcacaagcc cagcaacacc aaggtggaca 2200

agaaagttga gcccaaatct tgtgacaaaa ctcacactag tccaccgtct 2250

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa 2300

acccaaggac accctcatga tctcccggac ccctgaggtc acatgcgtgg 2350

tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 2400

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta 2450

caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 2500

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 2550

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc 2600

acaggtgtac accctgcccc catcccggga agagatgacc aagaaccagg 2650

tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 2700

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc 2750

cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 2800

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 2850

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg 2900

taaataagca tgcgacggcc ctagagtccc taacgctcgg ttgccgccgg 2950

gcgtttttta ttgttaactc atgtttgaca gcttatcatc gataagcttt 3000

<210> 20
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF light chain

<400> 20

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1				5				10						15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser
			20					25						30
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
			35					40						45
Cys	Arg	Ala	Ser	Arg	Asp	Ile	Lys	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln
			50					55						60
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Tyr	Ala	Thr
			65					70						75
Ser	Leu	Ala	Glu	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
			80					85						90
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
			95					100						105
Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	His	Gly	Glu	Ser	Pro	Trp	Thr
								33						

```
                110                 115                 120

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
                125                 130                 135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                140                 145                 150

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
                155                 160                 165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                170                 175                 180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                185                 190                 195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
                200                 205                 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                215                 220                 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                230                 235

<210> 21
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TF heavy chain

<400> 21
 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
   1               5                  10                  15

 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
                  20                  25                  30

 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                  35                  40                  45

 Ala Ala Ser Gly Phe Asn Ile Lys Glu Tyr Tyr Met His Trp Val
                  50                  55                  60

 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Leu Ile Asp
                  65                  70                  75

 Pro Glu Gln Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln Asp Arg
                  80                  85                  90

 Ala Thr Ile Ser Ala Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                  95                 100                 105
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Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                110                 115                 120

Arg Asp Thr Ala Ala Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                125                 130                 135

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                140                 145                 150

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                155                 160                 165

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                170                 175                 180

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                185                 190                 195

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                200                 205                 210

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
                215                 220                 225

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
                230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                260                 265                 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
                290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                305                 310                 315

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                320                 325                 330

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                335                 340                 345

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                350                 355                 360

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                365                 370                 375

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                380                 385                 390
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Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
395 400 405

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
410 415 420

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
425 430 435

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
440 445 450

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
455 460 465

Leu Ser Pro Gly Lys
470

<210> 22
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 22
caaatcttgt gacaaaactc acactagtcc accgtctcca gcac 44

<210> 23
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 23
tcgggtttag aacactgttt tgagtgtgat caggtggcag aggtc 45

<210> 24
<211> 63
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 24
cccaccgtcg ccggcacctg aactcctggg gggaccgtca gtcttcctct 50

tccccccaaa acc 63

<210> 25
<211> 71

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 25
gtacgggtgg cagcggccgt ggacttgagg acccccctgg cagtcagaag 50

gagaaggggg gttttgggtt c 71

<210> 26
<211> 63
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 26
cccaccgtcg ccggcacctg aactcctggg gggaccgtca gtcttcctct 50

tccccccaaa acc 63

<210> 27
<211> 71
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 27
gtacgggtgg cagcggccgt ggacttgagg acccccctgg cagtcagaag 50

gagaaggggg gttttgggtt c 71

<210> 28
<211> 67
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 28
ctagtccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 50

ctcttccccc caaaacc 67

<210> 29
<211> 67
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic

<400> 29
aggtggcacg ggtcgtggac ttgaggaccc ccctggcagt cagaaggaga 50

agggggttt tgggttc 67

<210> 30
<211> 67
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 30
ctagtccacc gtgcccagca cctgaactcc tgggggacc gtcagtcttc 50

ctcttccccc caaaacc 67

<210> 31
<211> 67
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 31
aggtggcacg ggtcgtggac ttgaggaccc ccctggcagt cagaaggaga 50

agggggttt tgggttc 67

<210> 32
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 32
tagctacaaa cgcgtatgcc tcgaagttaa aagtgcctga actg 44

<210> 33
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 33
gctgaaatgg gccccacatg cacggaggtg ttgaaaga 38

<210> 34

<211> 62
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 34
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